



PCT

RAW SEQUENCE LISTING

DATE: 09/09/2004

PATENT APPLICATION: US/10/506,455

TIME: 16:17:57

Input Set : A:\X-15648.ST25.txt

Output Set: N:\CRF4\09092004\J506455.raw

3 <110> APPLICANT: Beals, John
 4 Kuchibhotla, Uma
 6 <120> TITLE OF INVENTION: HETEROLOGOUS G-CSF FUSION PROTEINS
 8 <130> FILE REFERENCE: X-15648
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/506,455
 C--> 10 <141> CURRENT FILING DATE: 2004-08-31
 10 <150> PRIOR APPLICATION NUMBER: PCT/US03/03120
 11 <151> PRIOR FILING DATE: 2003-02-21
 13 <160> NUMBER OF SEQ ID NOS: 66
 15 <170> SOFTWARE: PatentIn version 3.2
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 174
 19 <212> TYPE: PRT
 20 <213> ORGANISM: Artificial Sequence
 22 <220> FEATURE:
 23 <223> OTHER INFORMATION: synthetic construct
 26 <220> FEATURE:
 27 <221> NAME/KEY: MISC_FEATURE
 28 <222> LOCATION: (17)..(17)
 29 <223> OTHER INFORMATION: Xaa at position 17 is Cys, Ala, Leu, Ser, or Glu;
 31 <220> FEATURE:
 32 <221> NAME/KEY: MISC_FEATURE
 33 <222> LOCATION: (37)..(37)
 34 <223> OTHER INFORMATION: Xaa at position 37 is Ala or Asn;
 36 <220> FEATURE:
 37 <221> NAME/KEY: MISC_FEATURE
 38 <222> LOCATION: (38)..(38)
 39 <223> OTHER INFORMATION: Xaa at position 38 is Thr, or any other amino acid exept Pro;
 41 <220> FEATURE:
 42 <221> NAME/KEY: MISC_FEATURE
 43 <222> LOCATION: (39)..(39)
 44 <223> OTHER INFORMATION: Xaa at position 39 is Tyr, Thr, or Ser;
 46 <220> FEATURE:
 47 <221> NAME/KEY: MISC_FEATURE
 48 <222> LOCATION: (57)..(57)
 49 <223> OTHER INFORMATION: Xaa at position 57 is Pro or Val;
 51 <220> FEATURE:
 52 <221> NAME/KEY: MISC_FEATURE
 53 <222> LOCATION: (58)..(58)
 54 <223> OTHER INFORMATION: Xaa at position 58 is Trp or Asn;
 56 <220> FEATURE:
 57 <221> NAME/KEY: MISC_FEATURE
 58 <222> LOCATION: (59)..(59)

ENTERED

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59 <223> OTHER INFORMATION: Xaa at position 59 is Ala or any other amino acid except Pro;
61 <220> FEATURE:
62 <221> NAME/KEY: MISC_FEATURE
63 <222> LOCATION: (60)..(60)
64 <223> OTHER INFORMATION: Xaa at position 60 is Pro, Thr, Asn, or Ser;
66 <220> FEATURE:
67 <221> NAME/KEY: MISC_FEATURE
68 <222> LOCATION: (61)..(61)
69 <223> OTHER INFORMATION: Xaa at position 61 is Leu, or any other amino acid except
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71 <220> FEATURE:
72 <221> NAME/KEY: MISC_FEATURE
73 <222> LOCATION: (62)..(62)
74 <223> OTHER INFORMATION: Xaa at position 62 is Ser or Thr;
76 <220> FEATURE:
77 <221> NAME/KEY: MISC_FEATURE
78 <222> LOCATION: (63)..(63)
79 <223> OTHER INFORMATION: Xaa at position 63 Ser or Asn;
81 <220> FEATURE:
82 <221> NAME/KEY: MISC_FEATURE
83 <222> LOCATION: (64)..(64)
84 <223> OTHER INFORMATION: Xaa at position 64 is Cys or any other amino acid except Pro;
86 <220> FEATURE:
87 <221> NAME/KEY: MISC_FEATURE
88 <222> LOCATION: (65)..(65)
89 <223> OTHER INFORMATION: Xaa at position 65 is Pro, Ser, or Thr;
91 <220> FEATURE:
92 <221> NAME/KEY: MISC_FEATURE
93 <222> LOCATION: (66)..(66)
94 <223> OTHER INFORMATION: Xaa at position 66 is Ser or Thr;
96 <220> FEATURE:
97 <221> NAME/KEY: MISC_FEATURE
98 <222> LOCATION: (67)..(67)
99 <223> OTHER INFORMATION: Xaa at position 67 is Gln or Asn;
101 <220> FEATURE:
102 <221> NAME/KEY: MISC_FEATURE
103 <222> LOCATION: (68)..(68)
104 <223> OTHER INFORMATION: Xaa at position 68 is Ala or any other amino acid except
Pro;
106 <220> FEATURE:
107 <221> NAME/KEY: MISC_FEATURE
108 <222> LOCATION: (69)..(69)
109 <223> OTHER INFORMATION: Xaa at position 69 is Leu, Thr, or Ser;
111 <220> FEATURE:
112 <221> NAME/KEY: MISC_FEATURE
113 <222> LOCATION: (93)..(93)
114 <223> OTHER INFORMATION: Xaa at position 93 is Glu or Asn;
116 <220> FEATURE:
117 <221> NAME/KEY: MISC_FEATURE
118 <222> LOCATION: (94)..(94)
119 <223> OTHER INFORMATION: Xaa at position 94 is Gly or any other amino acid except
Pro;

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121 <220> FEATURE:
122 <221> NAME/KEY: MISC_FEATURE
123 <222> LOCATION: (95)..(95)
124 <223> OTHER INFORMATION: Xaa at position 95 is Ile, Asn, Ser, or Thr;
126 <220> FEATURE:
127 <221> NAME/KEY: MISC_FEATURE
128 <222> LOCATION: (97)..(97)
129 <223> OTHER INFORMATION: Xaa at position 97 is Pro, Ser, Thr, or Asn;
131 <220> FEATURE:
132 <221> NAME/KEY: MISC_FEATURE
133 <222> LOCATION: (133)..(133)
134 <223> OTHER INFORMATION: Xaa at position 133 is Thr or Asn;
136 <220> FEATURE:
137 <221> NAME/KEY: MISC_FEATURE
138 <222> LOCATION: (134)..(134)
139 <223> OTHER INFORMATION: Xaa at position 134 is Gln or any other amino acid except
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141 <220> FEATURE:
142 <221> NAME/KEY: MISC_FEATURE
143 <222> LOCATION: (135)..(135)
144 <223> OTHER INFORMATION: Xaa at position 135 is Gly, Ser, or Thr;
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147 <221> NAME/KEY: MISC_FEATURE
148 <222> LOCATION: (141)..(141)
149 <223> OTHER INFORMATION: Xaa at position 141 is Ala or Asn;
151 <220> FEATURE:
152 <221> NAME/KEY: MISC_FEATURE
153 <222> LOCATION: (142)..(142)
154 <223> OTHER INFORMATION: Xaa at position 142 is Ser or any other amino acid except
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156 <220> FEATURE:
157 <221> NAME/KEY: MISC_FEATURE
158 <222> LOCATION: (143)..(143)
159 <223> OTHER INFORMATION: Xaa at position 143 is Ala, Ser, or Thr.
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163 Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
164 1 5 10 15
W--> 167 Xaa Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
168 20 25 30
171 Glu Lys Leu Cys Xaa Xaa Xaa Lys Leu Cys His Pro Glu Glu Leu Val
172 35 40 45
175 Leu Leu Gly His Ser Leu Gly Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
176 50 55 60
179 Xaa Xaa Xaa Xaa Xaa Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
180 65 70 75 80
183 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Xaa Xaa Xaa Ser
184 85 90 95
187 Xaa Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
188 100 105 110
191 Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
192 115 120 125

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195 Ala Leu Gln Pro Xaa Xaa Xaa Ala Met Pro Ala Phe Xaa Xaa Xaa Phe
196      130                      135                      140
199 Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
200 145                      150                      155                      160
203 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
204                      165                      170
207 <210> SEQ ID NO: 2
208 <211> LENGTH: 1044
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: synthetic construct
215 <400> SEQUENCE: 2
216 acccccctgg gccctgccag ctccctgccc cagagcttcc tgctcaagtg gggggaccgc      60
218 ggacggtcga gggacggggt ctccaaggac gagttcgctt tagagcaagt gaggaagatc      120
220 cagggcgatg gcgcagcgct ccagcggaat ctcgttcact ccttctaggt cccgctaccg      180
222 cgtcgcgagg tcgagaagct gtgtgccacc tacaagctgt gccaccccga ggagctggtg      240
224 ctcttcgaca cacggtggat gttcgacacg gtggggctcc tcgaccacct gctcggacac      300
226 tctctgggca tcccctgggc tcccctgagc agctgcgacg agcctgtgac agaccgtag      360
228 gggacccgag gggactcgtc gacgcccagc caggccctgc agctggcagg ctgcttgagc      420
230 caactccata gcgggtcggg ccgggacgtc gaccgtccga cgaactcggg tgaggtatcg      480
232 ggcccttttc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag      540
234 atggtccccg aggacgtccg ggaccttccc tagaggcccc agttgggtcc caccttggac      600
236 aactgcagc tggacgtcgc cgacgggctc aaccagggtt ggaacctgtg tgacgtcgac      660
238 ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggccct      720
240 aaacggtggt ggtagaccgt cgtctacctt cttagaccct accggggagc cctgcagccc      780
242 aaccagaccg ccatgccggc cttcgcctct gctttccggg acgtcgggtt ggtctggcgg      840
244 tacggccgga agcggagacg aaagcagcgc cgggcaggag gggtcctggt tgcctcccat      900
246 ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag      960
248 ctggaggtgt cgtaccgcgt cttaaggcac cttagccagc ccgacctcca cagcatggcg      1020
250 cagaattccg tgaacgggt cggg                                1044
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255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: synthetic construct
261 <400> SEQUENCE: 3
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264 ggacggtcga gggacggggt ctccaaggac gagttcgctt tagagcaagt gaggaagatc      120
266 cagggcgatg gcgcagcgct ccagcggaat ctcgttcact ccttctaggt cccgctaccg      180
268 cgtcgcgagg tcgagaagct gtgtgccacc tacaagctgt gccaccccga ggagctggtg      240
270 ctcttcgaca cacggtggat gttcgacacg gtggggctcc tcgaccacct gctcggacac      300
272 tctctgggca tcccctgggc tcccctgagc agctgcgacg agcctgtgac agaccgtag      360
274 gggacccgag gggactcgtc gacgcccagc caggccctgc agctggcagg ctgcttgagc      420
276 caactccata gcgggtcggg ccgggacgtc gaccgtccga cgaactcggg tgaggtatcg      480
278 ggcccttttc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag      540
280 atggtccccg aggacgtccg ggaccttccc tagaggcccc agttgggtcc caccttggac      600
282 aactgcagc tggacgtcgc cgacgggctc aaccagggtt ggaacctgtg tgacgtcgac      660

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284 ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggccctt 720
286 aaacggtggt ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc 780
288 acccaggggtg ccatgccggc cttcaactct accttccggg acgtcgggtg ggtccacagg 840
290 tacggccgga agttgagatg gaagcagcgc cgggcaggag gggctcctgg tgctcccat 900
292 ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag 960
294 ctggaggtgt cgtaccgcgt cttaaggcac cttgcccagc ccgacctcca cagcatggcg 1020
296 cagaattccg tggaaacgggt cggg 1044

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299 <210> SEQ ID NO: 4

300 <211> LENGTH: 1044

301 <212> TYPE: DNA

302 <213> ORGANISM: Artificial Sequence

304 <220> FEATURE:

305 <223> OTHER INFORMATION: synthetic construct

307 <400> SEQUENCE: 4

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308 acccccctgg gccctgccag ctccctgccc cagagcttcc tgctcaagtg gggggaccgc 60
310 ggacggtcga gggacggggt ctccaaggac gagttcgctt tagagcaagt gaggaagatc 120
312 cagggcgatg gcgcagcgct ccagcggaat ctcgttcact ccttctaggt cccgctaccg 180
314 cgtcgcgagg tcgagaagct gtgtaacacc accaagctgt gccaccccga ggagctgggtg 240
316 ctcttcgaca catttgtggtg gttcgacacg gtggggctcc tcgaccacct gctcggacac 300
318 tctctgggca tcccctgggc tcccctgagc agctgcgacg agcctgtgac agaccgtag 360
320 gggacccgag gggactcgtc gacgcccagc caggccctgc agctggcagg ctgcttgagc 420
322 caactccata gcgggtcggt ccgggacgtc gaccgtccga cgaactcggt tgaggatcgc 480
324 ggccctttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag 540
326 atggtccccg aggacgtccg ggaccttccc tagaggcccc agttgggtcc caccttggac 600
328 aactgcagc tggacgtcgc cgacgggctc aaccagggtt ggaacctgtg tgacgtcgac 660
330 ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggccctt 720
332 aaacggtggt ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc 780
334 acccaggggtg ccatgccggc cttcgctctt gctttccggg acgtcgggtg ggtccacagg 840
336 tacggccgga agcggagacg aaagcagcgc cgggcaggag gggctcctgg tgctcccat 900
338 ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag 960
340 ctggaggtgt cgtaccgcgt cttaaggcac cttgcccagc ccgacctcca cagcatggcg 1020
342 cagaattccg tggaaacgggt cggg 1044

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345 <210> SEQ ID NO: 5

346 <211> LENGTH: 1044

347 <212> TYPE: DNA

348 <213> ORGANISM: Artificial Sequence

350 <220> FEATURE:

351 <223> OTHER INFORMATION: synthetic construct

353 <400> SEQUENCE: 5

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354 acccccctgg gccctgccag ctccctgccc cagagcttcc tgctcaagtg gggggaccgc 60
356 ggacggtcga gggacggggt ctccaaggac gagttcgctt tagagcaagt gaggaagatc 120
358 cagggcgatg gcgcagcgct ccagcggaat ctcgttcact ccttctaggt cccgctaccg 180
360 cgtcgcgagg tcgagaagct gtgtgccacc tacaagctgt gccaccccga ggagctgggtg 240
362 ctcttcgaca cacggtggat gttcgacacg gtggggctcc tcgaccacct gctcggacac 300
364 tctctgggca tcccctgggc taactactagc agctgcgacg agcctgtgac agaccgtag 360
366 gggacccgat tggactcctc gacgcccagc caggccctgc agctggcagg ctgcttgagc 420
368 caactccata gcgggtcggt ccgggacgtc gaccgtccga cgaactcggt tgaggatcgc 480
370 ggccctttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag 540
372 atggtccccg aggacgtccg ggaccttccc tagaggcccc agttgggtcc caccttggac 600

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RAW SEQUENCE LISTING ERROR SUMMARY
 PATENT APPLICATION: US/10/506,455

DATE: 09/09/2004
 TIME: 16:17:58

Input Set : A:\X-15648.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 17, 37, 38, 39, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 93, 94
 Seq#:1; Xaa Pos. 95, 97, 133, 134, 135, 141, 142, 143

VERIFICATION SUMMARY

PATENT APPLICATION: **US/10/506,455**

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Input Set : **A:\X-15648.ST25.txt**

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16

M:341 Repeated in SeqNo=1